

FIGURE 1

HSP 90-beta (Mouse)  
SEQ ID NO:1

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1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskl dsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkdeekpki edvgsdeedd sgdkkkkkk kikekyidge elnktkpiwt rnpdditgee
301 ygefykslt n dwedhlavkh fsveggqlefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssppc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfs l edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-beta (Human)  
SEQ ID NO:2

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1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskl dsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkhsqfig ypitlyleke rekeisddea eeekgekeee
241 dkdeekpki edvgsdeedd sgdkkkkkk kikekyidge elnktkpiwt rnpdditgee
301 ygefykslt n dwedhlavkh fsveggqlefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepiday cvqqlkefdg kslsvstkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssppc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeadkndka vkdlvllfe
661 tallssgfs l edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 90-alpha (Human)  
SEQ ID NO:3

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1 mpeetqtqdg pmeeeevetf afqaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipnkqdrtilt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnddegy awessaggsf tvrtdtgepm
181 grgtkvilhl kedqteylee rriikeivkhh sqfigypitl fvekerdkev sddeaeeked
241 keeekkeek esedkpeied vgsdeeeekk dgdkkkkkki kekyidgeel nktkpiwtrn
301 pdditneeyg efyksltndw edhlavkhfs vegglefral lfvprapfd lfenrkkknn
361 iklyvrrvfi mdnceelipe ylnfirgvvd sedlplnlsr emlqgskilk virknlvkkc
421 lelftelaed kenyykfyeg fskniklgi edsqrkkls ellryysas gdemvslkdy
481 ctrmkengkh iyyitgetkd qvansafver lrxhgleviy miepidaycv qqlkefegkt
541 lsvstkegle lpedeeekkk geekktkfen lckimkdile kkvekvvsn rlvstspcciv
601 tstygtanm erimkaqalr dnstmgymaa kkhleinpdh sietlrqka eadkndksvk
661 dlvillyeta llssgfsled pqthanriyr miklglgide ddptaddtsa avteempple
721 gddtsrmee vd

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HSP 84 (Mouse)  
SEQ ID NO:4

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1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkksqfig ypitlyleke rekeisddea eeekgekeee
241 dkedeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepidey cvqqlkefdg kslsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivotlrq kaeadkndka vkdlvllife
661 tallssgfsl edpqthsnri yrmiklglgi dedevtaeep saavpdeipp legdedasrm
721 eevd

```

HSP 84 (Human)  
SEQ ID NO:5

```

1 mpeevhhgee evetfafgae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkksqfig ypitlyleke rekeisddea eeekgekeee
241 dkedeekpki edvgsdeedd sgdkkkkktk kikekyidqe elnktkpiwt rnpdditqee
301 ygefysltn dwedhlavkh fsvegglefr allfiprrap fdlfenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremllqgski lkvirknivk kclelfsela
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiyyitges keqvansafv ervrkrgefv vymtepidey cvqqlkefdg kslsvtkeg
541 lelpedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivotlrq kaeadkndka vkdlvllife
661 tallssgfsl edpqthsnri yrmiklglgi dedevaaeep naavpdeipp legdedasrm
721 eevd

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HSP 86 (Mouse)  
SEQ ID NO:6

```

1 mpeetqtqdg pmeeevetf afgaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhinl ipskqdrtilt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfgvgfys aylvaekvtv itkhnddegy awessaggsf tvrtdtgepm
181 grgtkvilhl kedqteylee rrikeivkkh sqfigypitl fvekerdkev sddeaeekke
241 keeekekeek esddkpeied vgsdeeeek kdgdkkkkkk ikekyidqee lnktkpiwtr
301 npdditneey gefyksltn dwedhlavkh fsvegglefra llfvprrapf dlfenrkkkn
361 niklyvrrvf imdnceelip eylnfirgv dsedlplnis remllqgski lkvirknivk
421 clelftelae dkenykkfy qfsknklgi hedsqnrkl sellrytsa sgdemvslkd
481 yctrmkengk hiyfitgetk dqvansafv rlrkhglevi ymiepidey cvqqlkefegk
541 tlsvtkegl elpedeeek kqeeektkfe nlckimkdil ekkvekvvvs nrlvtspcci
601 vtstygtan merimkaqa lrdnstmgym akkhleinp hsiietlrq aeadkndksv
661 kdlvillyet allssgfsle dpqthanriy rmiklglgid eddptvddts aavteemppl
721 egddtsrme evd

```

HSP 86, HSP 60 (Human)  
SEQ ID NO:7

1 mlrlptvfrq mrpvsrvlap hltrayakdv kfgadaralm lggvdllada vavtmgpkgr  
61 tviieqswgs pkvtkdgvtv aksidldkky knigaklvqd vanntneeag dgtttatvla  
121 rsiakegfek iskganpvei rrgvmlavda viaelkkqsk pvttpeeiaq vatisangdk  
181 eigniidam kkvggrkgvit vkdgktlnde leiiegmkf d rgyispyfin tskggkcefq  
241 dayvllsekk issiqsiypa leianahrkp lviiaedvdg ealstlvlnr lkvglqvav  
301 kapgfgdnrk nqlkdmaiat ggavfgeegl tlnledvqph dlqkvgeviv tkddamllkg  
361 kgdkaqiekr iqeiieql dv ttseyekekl nerlaklsdg vavlkvggts ddevnekkdr  
421 vtdalnatra aveegivl gg gcallrcipa ldsltpaned qkigieiikr tlkipamtia  
481 knagvegsli vekimqssse vgydamagdf vnmvekgiid ptkvvrall daagvasllt  
541 taevvvteip keekdpmgga mggmggmgg gm f

L-plastin (Human)  
SEQ ID NO:8

1 margsvsdee mmelreafak vtdgngyis fneindlfka acplpgyrv reitenlmat  
61 gdldqdgri s fdefikifhg lkstdvaktf rkainkkegi caiggtseqs svgtqhsyse  
121 eekyafvwi nkalendpdc rhvipmnpnt ndlfnavgdg ivlckminls vpd tiderti  
181 nkkkltpfti qenlnlaln asaigchvvn igaedlkegk pylvlglwq vikiglfadi  
241 elsrnealia llregesled lmkl speell lrwanyhlen agcnkignfs tdikdskayy  
301 hll eqvapkg deegvpavvi dmsglrekdd igraecmlqq aerlgcrqfv tatdvvrngp  
361 klnlafianl fnrypalhkp enqdidwgal egetreertf rnwmnslgvn prvn hlysd l  
421 sdalvifgly ekikvpv dwn rvnkppypkl ggnmklenc nyavelgknq akfslvgigg  
481 qdlnegnrtl tlaliwqlmr rytlnileei gggqkvnddi ivnwvnetlr eaeksssis s  
541 fkdpkistsl pvldlidai q pgsinydllk tenlndekl nnakyaisma rkigarvya l  
601 pedlvevnpk mvmtvfac lm gkgmkrv

FIG. 2

EL4 Conditioned Media Repels T cells *in vitro*

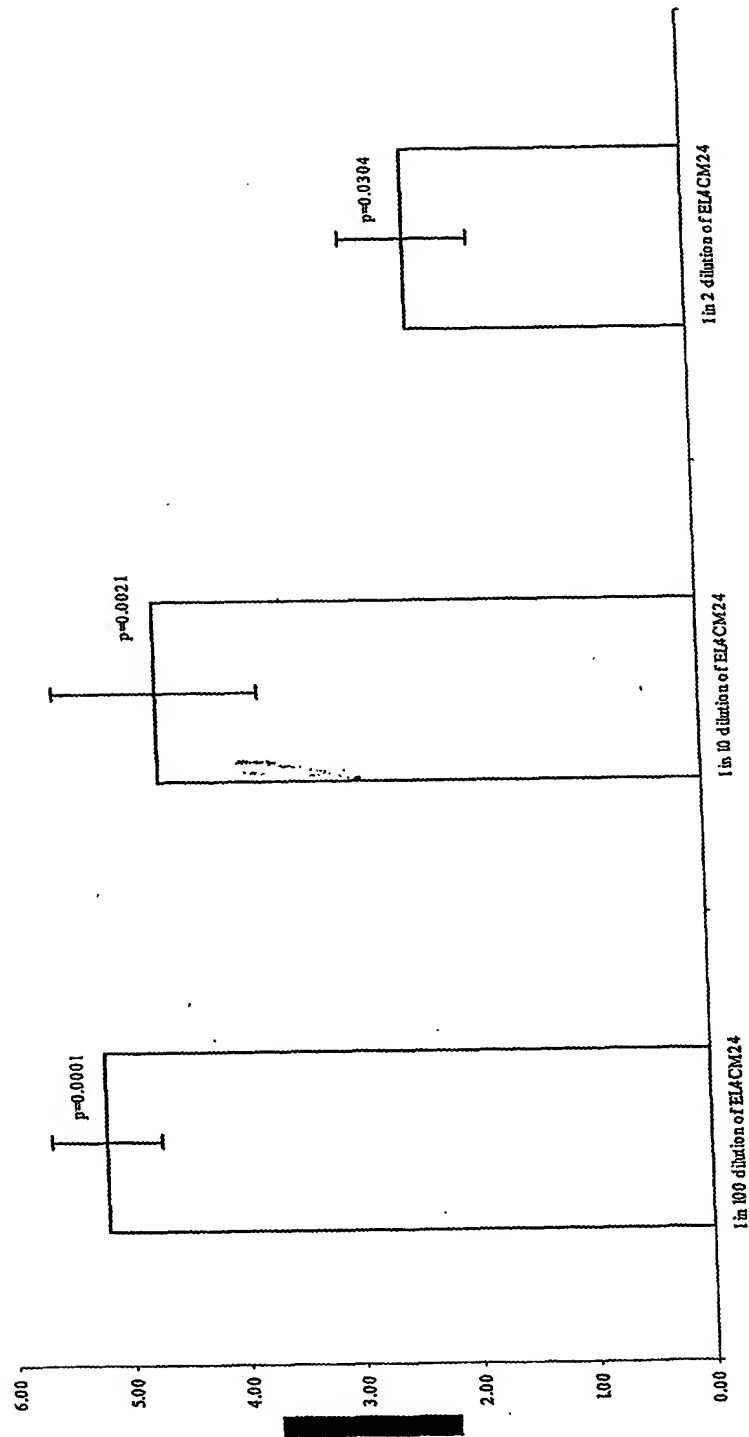
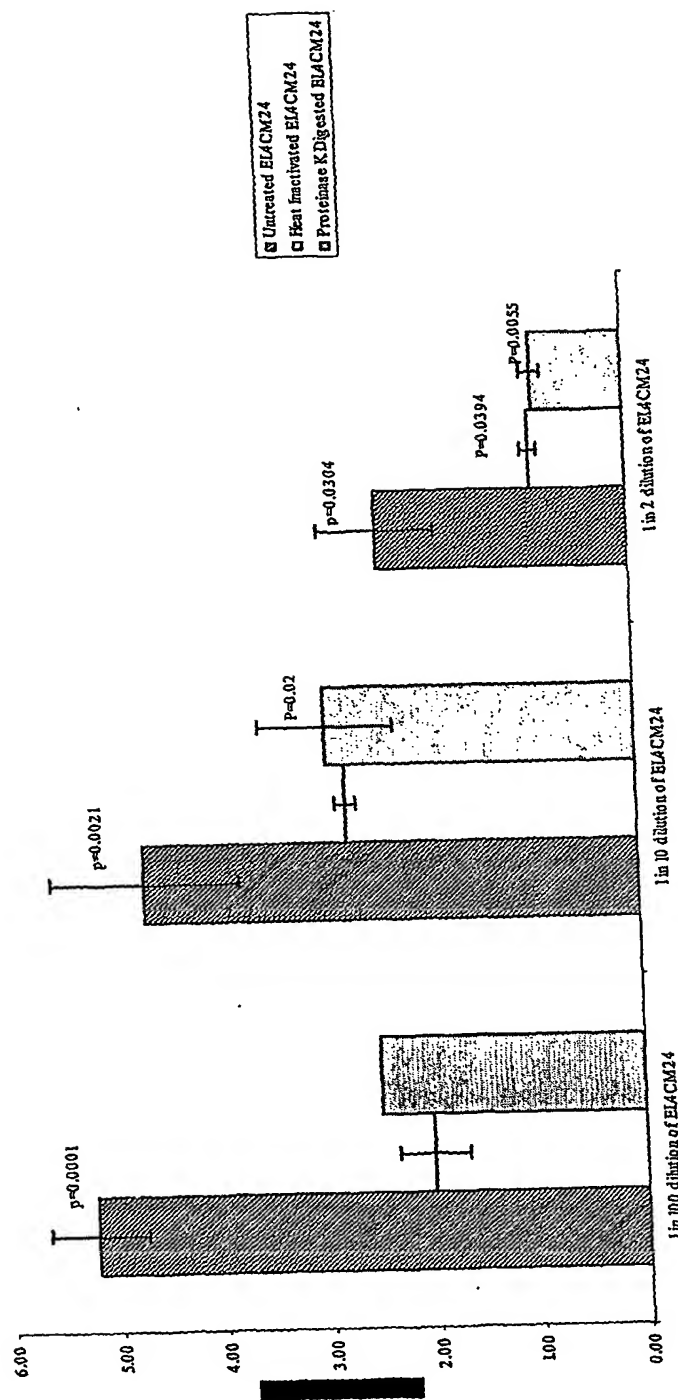


FIG. 3

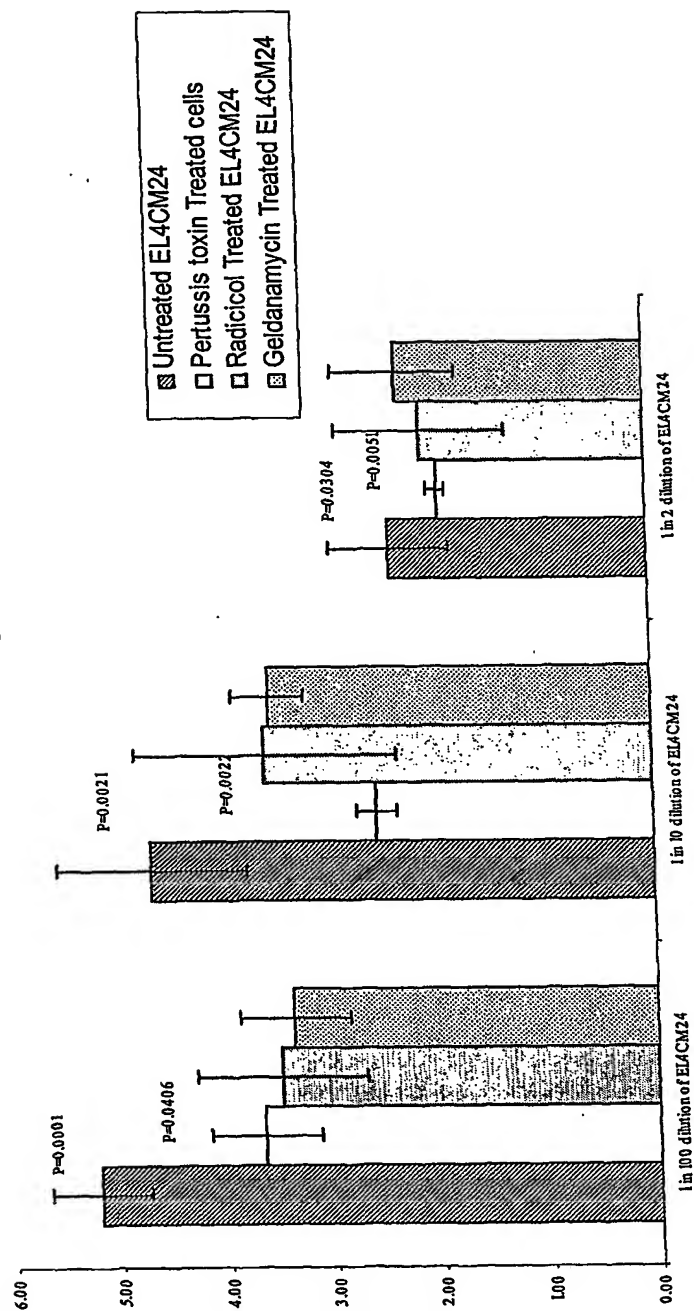
Heat Inactivation and Proteinase K Digestion of EL4CM24



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**FIG. 4**

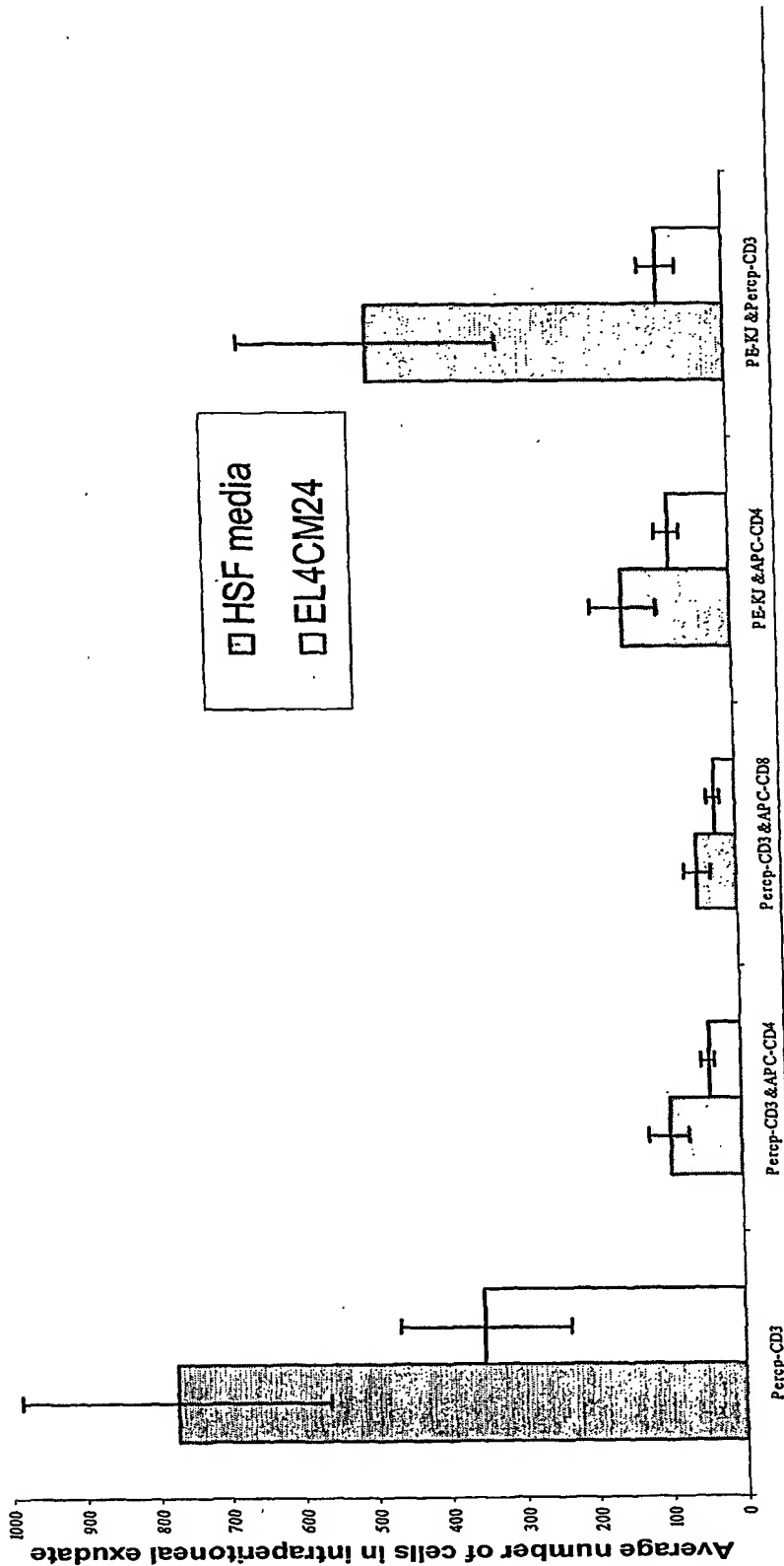
Use of Specific Inhibitors



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FIG. 5

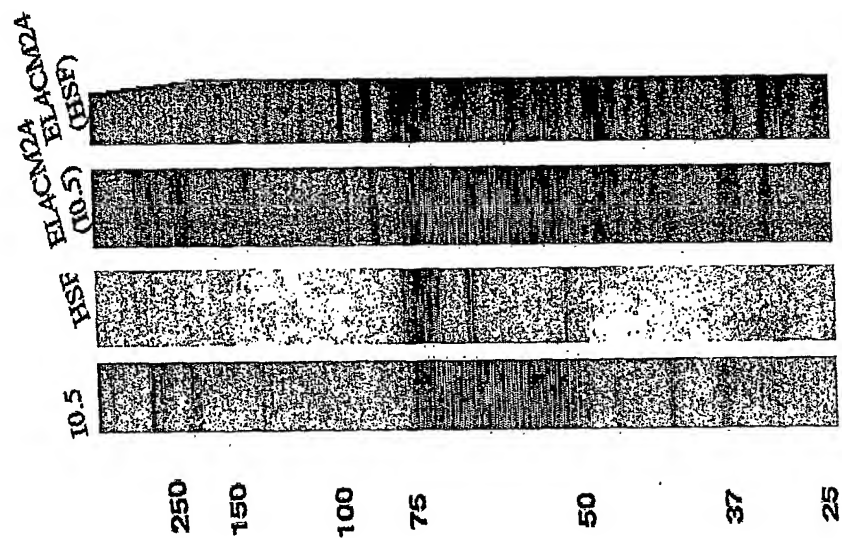
EL4 Conditioned Media Repels T cells *in vivo*



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**FIG. 6**

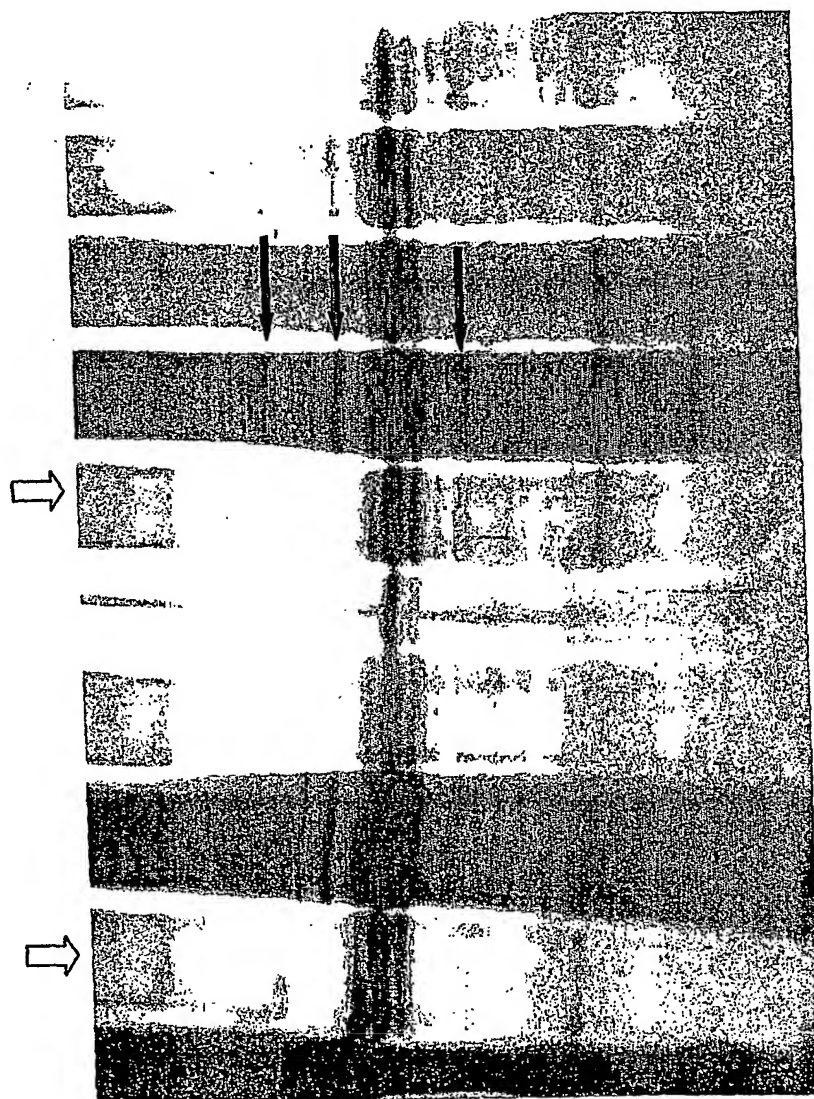
EL4CM24 SDS PAGE



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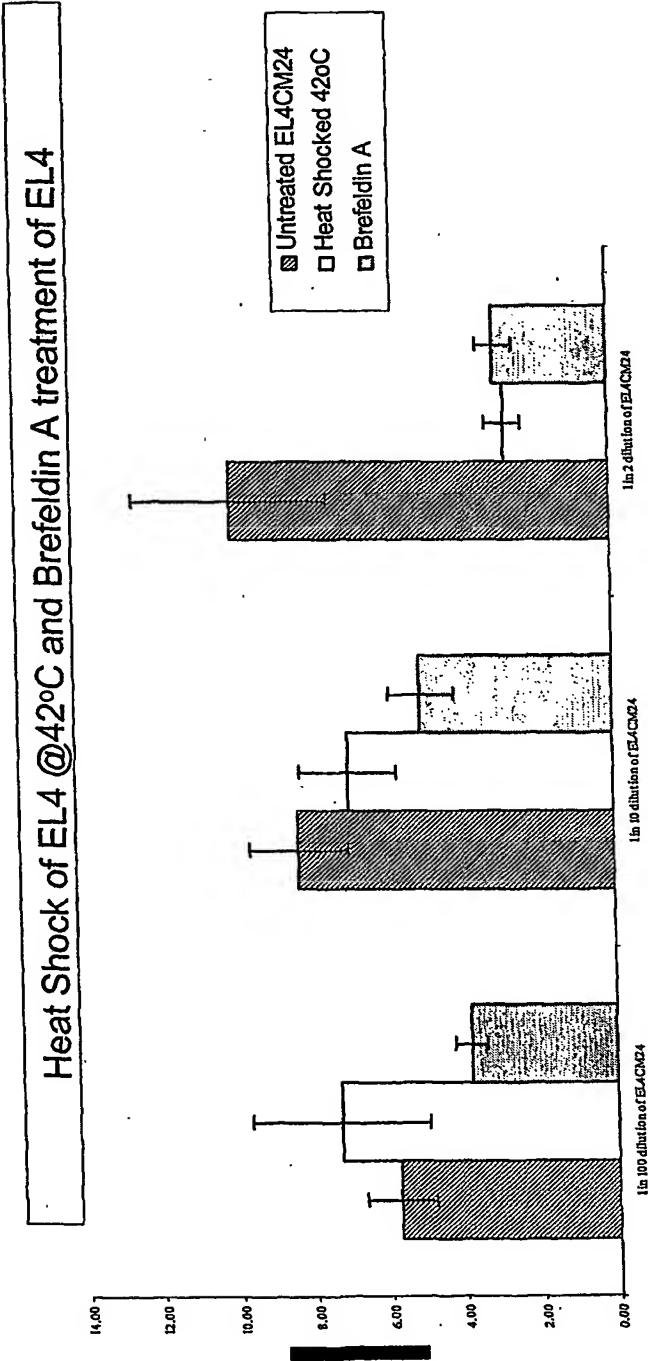
**FIG. 7**

**Ion Exchange Chromatography**



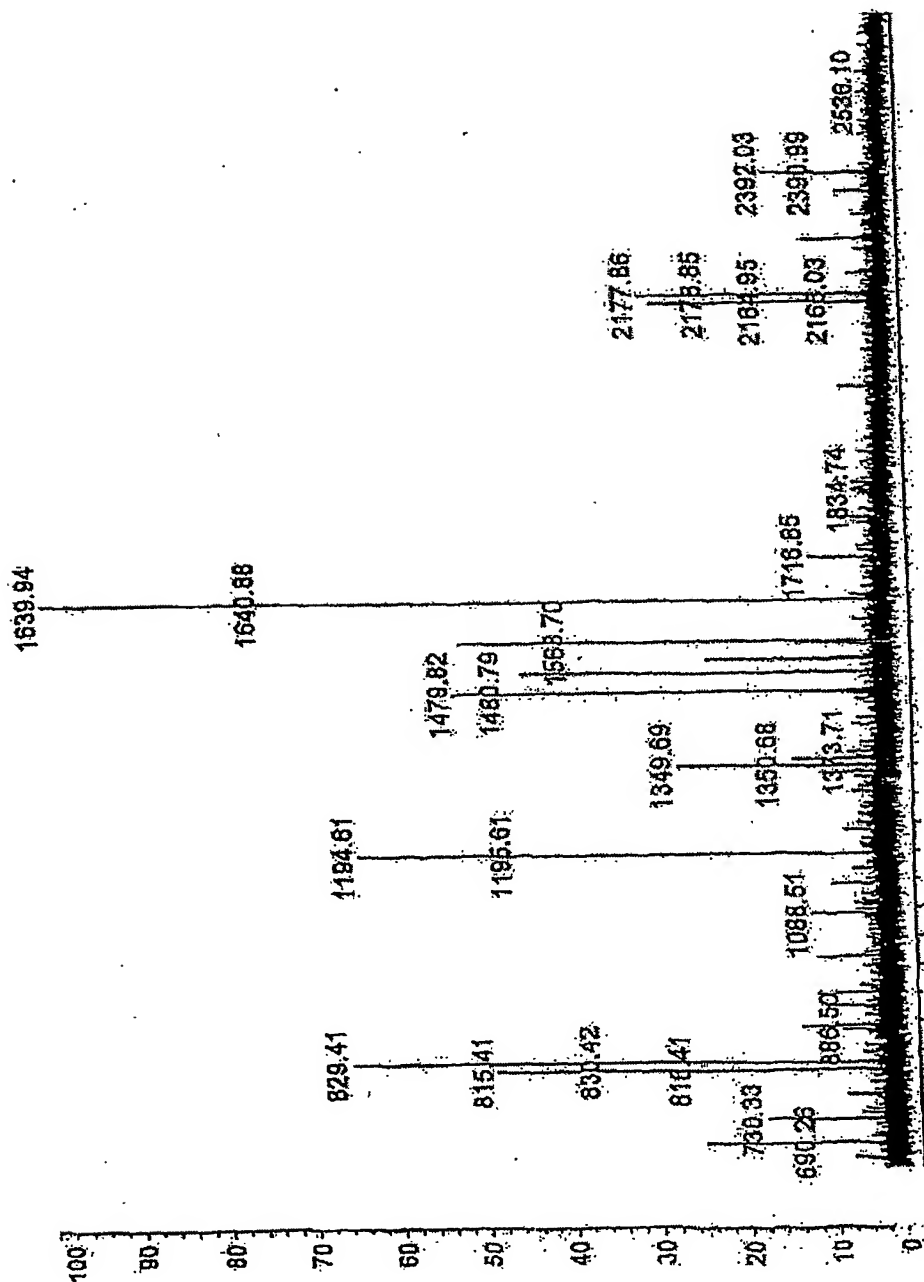
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FIG. 8



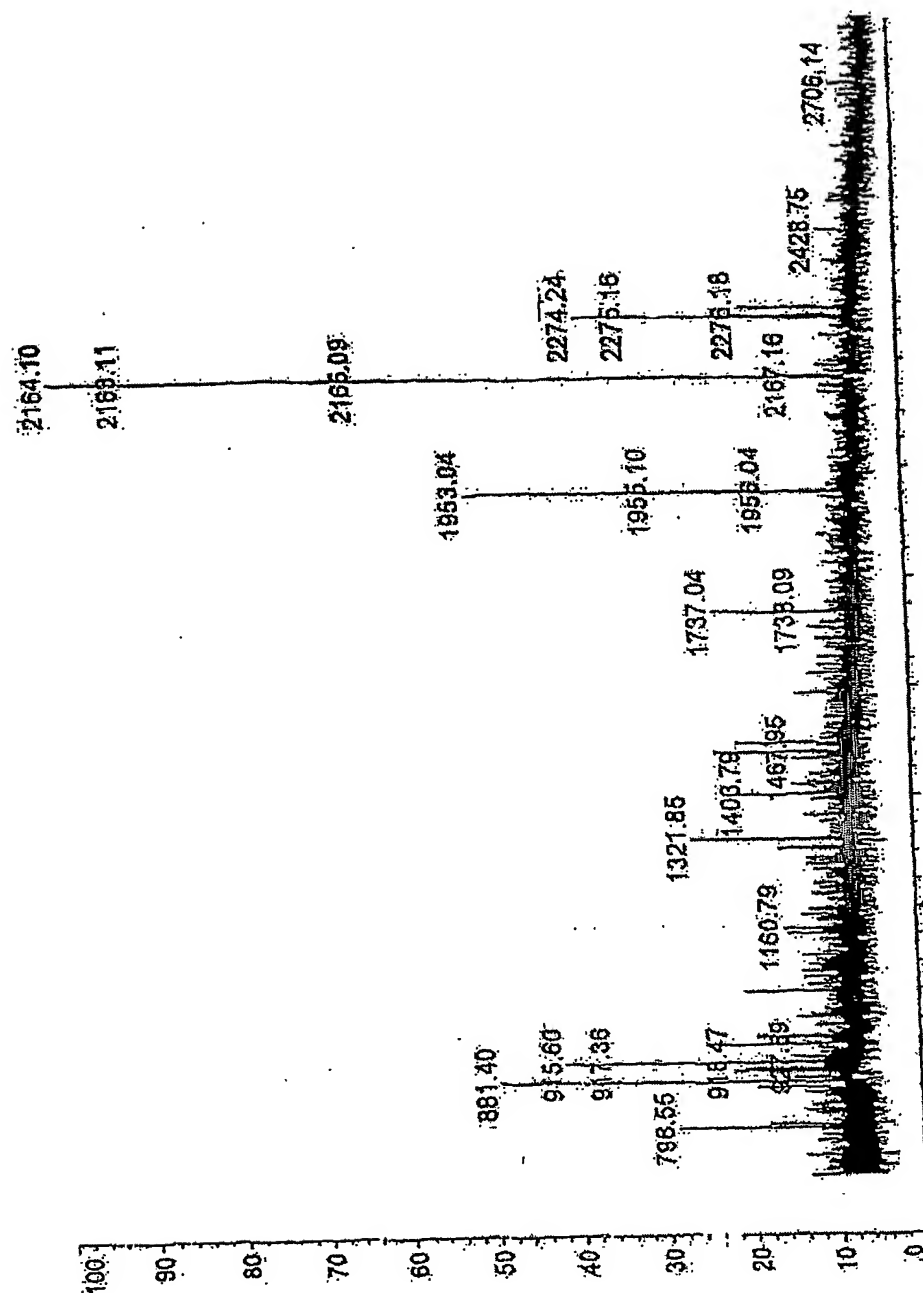
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FIG. 9



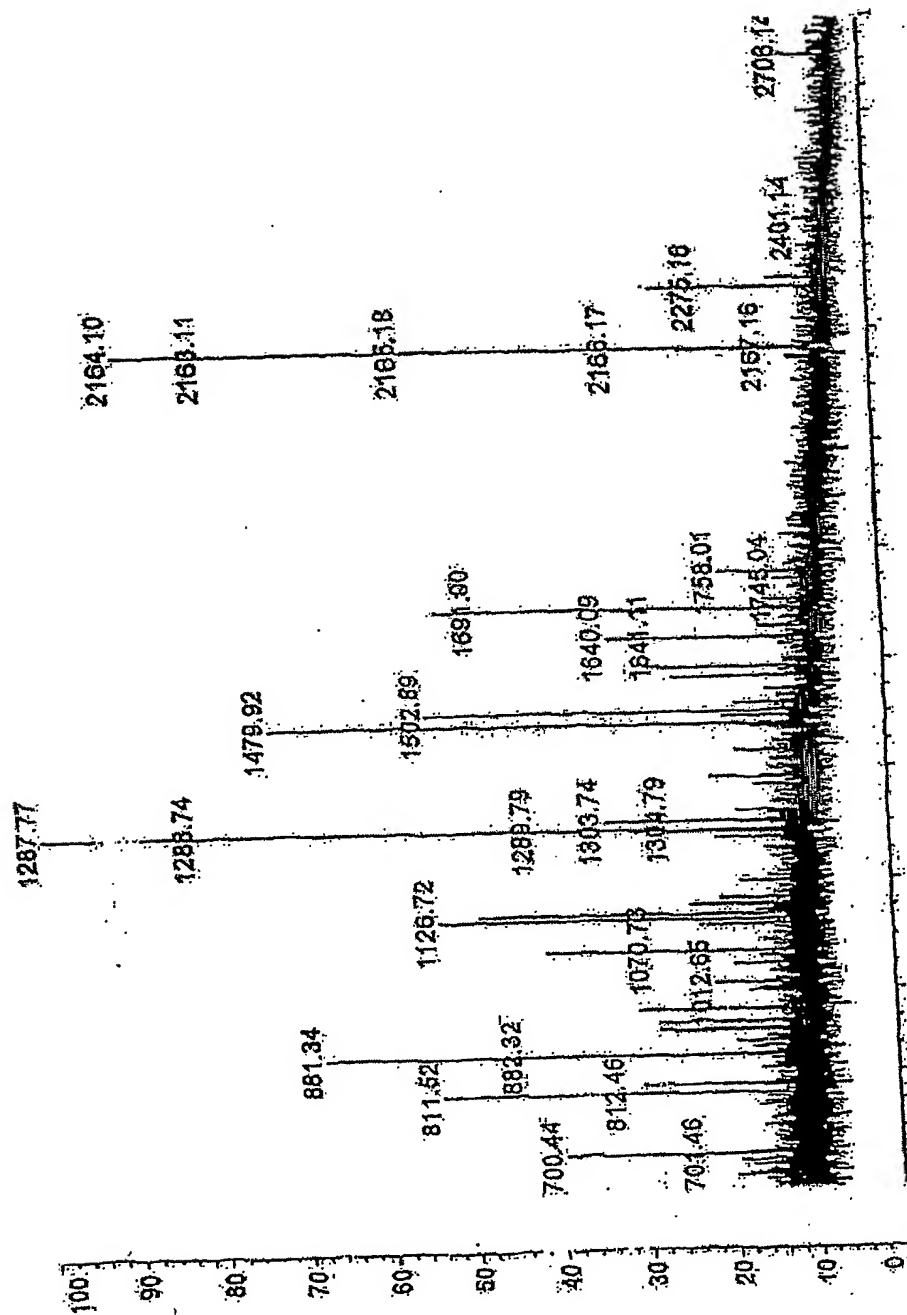
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FIG. 10



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FIG. 11



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## FIG. 12A

## MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest  
 Database searched: NCBI nr.121002  
 Molecular weight search (1000 - 100000 Da) selects 1195692 entries.  
 Full pI range: 1247039 entries.  
 Species search (MAMMALS) selects 197947 entries.  
 Combined molecular weight, pI and species searches select 186900 entries.  
 MS-Fit search selects 407 entries (results displayed for top 4 matches):

Considered modifications: [Peptide N-terminal Gln to pyroGln] Oxidation of M [Protein N-terminus Acetylated]

Min. # Peptides to Match	Peptide Mass Tolerance (+/-)	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N-terminus Hydrogen (H)	Peptide C-terminus Free Acid (O H)	Input # Peptide Masses IS
4	150.000 ppm			1				

## Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	7.02e+003	8/15 (53%)	81963.2 / 4.99	EQUUS CABALLUS	<u>20177936</u>	heat shock protein 90 beta
2	6.91e+003	8/15 (53%)	83264.6 / 4.97	HOMO SAPIENS	<u>20149594</u>	Unknown (protein for MGC:1138)
3	6.79e+003	8/15 (53%)	84843.9 / 5.26	HOMO SAPIENS	<u>11277141</u>	hypothetical protein
4	2.25e+003	7/15 (46%)	83316.8 / 5.06	RATTUS SP.	<u>1346320</u>	heat shock protein 90; hsp90

## Detailed Results

1. 8/15 matches (53%), 81963.2 Da, pI = 4.99, Acc. # 20177936, EQUUS CABALLUS, heat shock protein 90 beta.

m/z submitted	MR+ matched	Delta ppm	start and	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	570	575 (K)VTISNR(L)	
829.4100	829.5300	-144.6415	323	329 (R)ALLEFIPR(R)	
891.3500	891.4232	-84.4094	421	427 (K)EYEAESK(N)	
1194.6100	1194.6483	-32.0277	65	74 (K)IDHHPKQER(T)	
1348.6900	1348.6650	18.5557	312	322 (K)RFSVEGQLEFR(A)	
1513.7800	1513.7862	-4.1036	371	384 (R)GVVDSLEPLNISR(R)	
2176.8600	2176.9457	-39.5681	449	467 (R)YHTSQGDEMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	474	494 (K)SIYVITGESKEQVANSATVER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/713 AA's) of the protein.  
 Coverage Map for This Hit (MS-Digest Index #): 1205701

FIG. 12B

2. 8115 matches (33%), 83164.6 Da, pI = 4.97, Acc. # 29149394, HOMO SAPIENS, Unknown protein for MGC:1133).

m/z	MH <sup>+</sup>	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YVTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)FYRAERK(N)	
1194.6100	1194.6483	-32.0277	73 82	(K)DILFNPQER(T)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVRCOLEFRA(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSFYVR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SYVYTGSEKQVANSAEVSR(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (93/724 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest Index #): 137455

3. 8115 matches (33%), 83164.6 Da, pI = 5.26, Acc. # 11277141, HOMO SAPIENS, Hypothetical protein

m/z	MH <sup>+</sup>	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YVTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)FYRAERK(N)	
1194.6100	1194.6483	-32.0277	73 82	(K)DILFNPQER(T)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVRCOLEFRA(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSFYVR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SYVYTGSEKQVANSAEVSR(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 12% (93/737 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest Index #): 130126

4. 7115 matches (46%), 83164.6 Da, pI = 5.06, Acc. # 1346320, RATTUS SP., heat shock protein 90; hsp90.

m/z	MH <sup>+</sup>	Delta	start end	Peptide Sequence	Modification
submitted	matched	ppm			
689.3000	689.3946	-137.2410	578 583	(K)YVTSNR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	429 435	(K)FYRAERK(N)	
1194.6100	1194.6483	-32.0277	73 82	(K)DILFNPQER(T)	
1348.6900	1348.6650	18.5557	320 330	(K)HESVRCOLEFRA(A)	
1513.7800	1513.7862	-4.1036	379 391	(R)GVVDSKPLNISR(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)YHTSQSDPMISLSFYVR(Q)	
2390.9900	2391.1832	-80.8096	482 502	(K)SYVYTGSEKQVANSAEVSR(V)	

8 unmatched masses: 730.3300 815.4100 1194.6100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

## MS-Tag Search Results

Sample ID (contaminant): 494 A: 1040 AKPVEHLE

Database searched: NCBI nr.121002

Full Molecular Weight range: 1247039 entries

Full pI range: 1247039 entries

Species search: 1040 AKPVEHLE 191947 entries

Number of sequences passing through parent score filter: 4253

MS-Tag search select: 7 entries (results displayed for top 3 matches).

Parent mass: 1194.6100 (46.0200 Da)

Fragment ions used in search: 175.31, 212.00, 229.20, 343.61, 355.43, 512.43, 539.50, 616.31, 713.44, 740.56, 866.23 (46.050 Da)

Ion Types Considered: a b y z b1

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N-Terminus Hydrogen (H)	Peptide C-Terminus Free Acid (O H)
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## Result Summary

Rank	Unmatched Ions	Sequence	MH <sup>+</sup> Calculated (Da)	MH <sup>+</sup> Error (Da)	Protein MW (Da)	Species	NCBI#121002 Accession #	Protein Name
1	0/11	(K)DILFNPQER(T)	1194.6483	-0.0383	83213.77497	MOUSE	121881	Heat shock protein HSP 90-beta (HSP 90) (Tumor specific transmembrane 84 kDa subunit) (TSTA)
1	0/11	(K)DILFNPQER(T)	1194.6483	-0.0383	83364.17503	MUS MUSCULUS	669395	Heat shock protein, 84 kDa 1
1	0/11	(K)DILFNPQER(T)	1194.6483	-0.0383	14668.47444	HOMO SAPIENS	231110	Heat shock protein beta

## FIG. 12C

### Detailed Results

Rank	Unmatched Ions	Sequence	MH <sup>+</sup> Calculated (Da)	MH <sup>+</sup> Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	MS-Digest Index #	Protein Name
1	0/11	(K)DILNPQER(T)	1194.6483	-0.0383	83315.7/4.97	MOUSE	123681	518176	Heat shock protein HSP 90-beta (HSP 84) (Tumor specific transfection 84 kDa antigen) (TSTA)
2	0/11	(K)DILNPQER(T)	1194.6483	-0.0383	83361.1/5.03	MUS MUSCULUS	6680305	583990	heat shock protein, 84 kDa

Fragment-Ion (m/z)	175.31	212.00	229.20	242.62	335.43	512.43	529.50	625.31	723.44	740.58	966.73
Ion-type	b <sub>1</sub>	NP	b <sub>2</sub>	b <sub>3</sub>	PQE	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>4</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>6</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>6</sub>	γ <sub>8</sub>
Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19
			D1	D11							
			0.01	0.42							

Fragment-Ion (m/z)	175.31	212.00	229.20	242.62	335.43	512.43	529.50	625.31	723.44	740.58	966.73
Ion-type	b <sub>1</sub>	NP	b <sub>2</sub>	b <sub>3</sub>	PQE	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>4</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>6</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>6</sub>	γ <sub>8</sub>
Delta Da	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19
			D1	D11							
			0.01	0.42							

### MS-Tag Search Results

Sample ID (comment): Apo A-1 1040 AKPVLEDLR  
 Database searched: NCBI nr.121002  
 Molecular weight search (1000 - 100000 Da) selects 1195697 entries.  
 Full pI range: 1147039 entries.  
 Species search (MAMMALS) selects 197947 entries.  
 Combined molecular weight, pI and species searches select 186900 entries.  
 Number of sequences passing through parent mass filter: 4989  
 MS-Tag search selects 18 entries (results displayed for top 3 matches).  
 Parent mass: 815.4100 (+/- 0.0000 Da)  
 Fragment ions used in search: 185.26, 255.27, 272.34, 298.32, 354.45, 371.53, 417.39, 445.25, 518.35 (+/- 0.50 Da)  
 Ion Types Considered: a b y n h i

Search Mode	Max. # Unmatched Ions	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O H)
Identity	1		Trypsin	1			

### Result Summary

Rank	Unmatched Ions	Sequence	MH <sup>+</sup> Calculated (Da)	MH <sup>+</sup> Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	Protein Name
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	75541.0/5.28	MUS MUSCULUS	20882565	similar to heat shock protein 86
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	84674.2/4.94	HOMO SAPIENS	123678	90 kDa heat-shock protein (AA 1-732)
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	57068.0/6.38	HOMO SAPIENS	12804541	hypothetical protein LOC63929

### Detailed Results

Rank	Unmatched Ions	Sequence	MH <sup>+</sup> Calculated (Da)	MH <sup>+</sup> Error (Da)	Protein MW (Da)/pI	Species	NCBI nr.121002 Accession #	MS-Digest Index #	Protein Name																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	75541.0/5.28	MUS MUSCULUS	20882565	515911	similar to heat shock protein 86																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	84674.2/4.94	HOMO SAPIENS	123678	162860	90 kDa heat-shock protein (AA 1-732)																														
<table border="1"> <tr> <td>Fragment-Ion (m/z)</td><td>185.26</td><td>255.27</td><td>272.34</td><td>298.32</td><td>354.45</td><td>371.53</td><td>417.39</td><td>445.25</td><td>518.35</td></tr> <tr> <td>Ion-type</td><td>b<sub>1</sub></td><td>γ<sub>2</sub>-NH<sub>3</sub><sup>+</sup></td><td>γ<sub>2</sub></td><td>b<sub>3</sub></td><td>γ<sub>5</sub>-NH<sub>3</sub><sup>+</sup></td><td>γ<sub>5</sub></td><td>b<sub>4</sub></td><td>b<sub>4</sub></td><td>γ<sub>8</sub></td></tr> <tr> <td>Delta Da</td><td>0.13</td><td>0.12</td><td>0.17</td><td>0.11</td><td>0.24</td><td>0.29</td><td>0.10</td><td>-0.03</td><td>0.04</td></tr> </table>										Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35	Ion-type	b <sub>1</sub>	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>2</sub>	b <sub>3</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>5</sub>	b <sub>4</sub>	b <sub>4</sub>	γ <sub>8</sub>	Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35																														
Ion-type	b <sub>1</sub>	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>2</sub>	b <sub>3</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>5</sub>	b <sub>4</sub>	b <sub>4</sub>	γ <sub>8</sub>																														
Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04																														
1	0/9	(K)ALLFVPR(R)	815.5143	-0.1043	57068.0/6.38	HOMO SAPIENS	12804541	171353	hypothetical protein LOC63929																														
<table border="1"> <tr> <td>Fragment-Ion (m/z)</td><td>185.26</td><td>255.27</td><td>272.34</td><td>298.32</td><td>354.45</td><td>371.53</td><td>417.39</td><td>445.25</td><td>518.35</td></tr> <tr> <td>Ion-type</td><td>b<sub>1</sub></td><td>γ<sub>2</sub>-NH<sub>3</sub><sup>+</sup></td><td>γ<sub>2</sub></td><td>b<sub>3</sub></td><td>γ<sub>5</sub>-NH<sub>3</sub><sup>+</sup></td><td>γ<sub>5</sub></td><td>b<sub>4</sub></td><td>b<sub>4</sub></td><td>γ<sub>8</sub></td></tr> <tr> <td>Delta Da</td><td>0.13</td><td>0.12</td><td>0.17</td><td>0.11</td><td>0.24</td><td>0.29</td><td>0.10</td><td>-0.03</td><td>0.04</td></tr> </table>										Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35	Ion-type	b <sub>1</sub>	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>2</sub>	b <sub>3</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>5</sub>	b <sub>4</sub>	b <sub>4</sub>	γ <sub>8</sub>	Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
Fragment-Ion (m/z)	185.26	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35																														
Ion-type	b <sub>1</sub>	γ <sub>2</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>2</sub>	b <sub>3</sub>	γ <sub>5</sub> -NH <sub>3</sub> <sup>+</sup>	γ <sub>5</sub>	b <sub>4</sub>	b <sub>4</sub>	γ <sub>8</sub>																														
Delta Da	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04																														

FIG. 13A

## MS-Fit Search Results

Sample ID (comment): Nitric Bullet digest  
 Database searched: NCBI nr.S1403  
 Molecular weight search (1000 - 100000 Da) selects 1421445 entries.  
 Full pI range: (432416 entries).  
 Species search (HUMAN RODENT) selects 214838 entries.  
 Combined molecular weight, pI and species searches select 222557 entries.  
 MS-Fit search selects 5 entries (results displayed for top 3 matches).

Considered modifications: 1 Peptide N-terminal Cln to pyroGlu | Oxidation of M | Protein N-terminus Acetylated |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (OH)	Input # Peptide Masses 13
7	150.000							

## Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.S1403 Accession #	Protein Name
1	1.81e+003	7/13 (53%)	94057.0 / 5.13	RATTUS NORVEGICUS	24025637	ischemia responsive 94 kDa protein
2	449	7/13 (53%)	94081.1 / 5.13	MUS MUSCULUS	13277753	heat shock protein 4
3	449	7/13 (53%)	94133.1 / 5.15	MUS MUSCULUS	6680301	apc-2

## Detailed Results

1. 7/13 matches (53%), 94057.0 Da, pI = 5.13, Acc. # 24025637, RATTUS NORVEGICUS, ischemia responsive 94 kDa protein.

m/z submitted	MW matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K)VLTEVR(K)	
949.6100	949.5219	92.7425	62	69	(K)NYVOGEKR(F)	
1323.8500	1323.7116	104.7200	222	234	(K)VLATAFDITLCGR(K)	
1402.7800	1402.6313	106.0213	619	629	(K)NAVEEYVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGQETIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EESITDVVPYFSLR(W)	
1953.0400	1952.8336	105.6759	406	421	(R)WNSPAEEGSSDCEVFPK(N)	

1 unmatched masses: 915.6000 917.3600 1305.8400 1478.8800 1587.9500 1624.0500

The matched peptides cover 10% (84/840 AA's) of the protein.  
 Coverage Map for This Hit (MS-Digest Index #): 787619

2. 7/13 matches (53%), 94081.1 Da, pI = 5.13, Acc. # 13277753, MUS MUSCULUS, heat shock protein 4

FIG. 13B

m/z submitted	MH <sup>+</sup> matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>YLTRYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGFKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGK</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDK</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVFPYISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest index #): 302745

2. 7/13 matches (53%), 94133.1 Da, pI = 5.15, Acc. # 6680301, MIIIS MUSCULUS, app. 2.

m/z submitted	MH <sup>+</sup> matched	Delta ppm	start	end	Peptide Sequence	Modifications
798.5500	798.4514	123.4893	431	436	(K) <u>YLTRYR</u> (K)	
949.6100	949.5219	92.7425	62	69	(K) <u>NTVOGFKR</u> (F)	
1305.8400	1305.7418	75.1849	670	680	(K) <u>QVYVDKLAELK</u> (S)	
1321.8500	1321.7116	104.7200	222	234	(K) <u>VLATAFDITLGGK</u> (K)	
1402.7800	1402.6313	106.0213	620	630	(K) <u>NAVEEYVYEMR</u> (D)	
1495.8400	1495.7029	91.6785	20	33	(R) <u>AGGIETIANEYSDK</u> (C)	
1736.0700	1735.9271	82.3407	391	405	(R) <u>EFSITDVVFPYISLR</u> (W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest index #): 1129227

## FIG. 14A

## MS-Fit Search Results

Sample ID (construct): Magic Bullet digest  
 Database searched: NCBI nr.51403  
 Molecular weight search (1000 - 100000 Da) selects 1372760 entries.  
 Full pf range: 1432416 entries.  
 Species search: (HUMAN RODENT) selects 224838 entries  
 Combined molecular weight, pf and species searches select 211465 entries.  
 MS-Fit search selects 335 entries (results displayed for top 3 matches).

Considered modifications: [ Peptide N-terminal C<sub>16</sub> to pyroGlu ] Oxidation of M [ Protein N-terminus Acetylated ]

Min. # Peptides to Match	Peptide Mass Tolerance (+/-) ppm	Peptide Masses are monoisotopic.	Digest Used Trypsin	Max. # Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O/H)	Input # Peptide Masses 17
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## Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr.51403 Accession #	Protein Name
1	1.22e+005	11/17 (64%)	70149.7 / 5.20	MUS MUSCULUS	<u>29840803</u>	unnamed protein product
2	1.22e+005	11/17 (64%)	70163.8 / 5.24	MUS MUSCULUS	<u>26326929</u>	unnamed protein product
3	2.66e+004	10/17 (58%)	70201.8 / 5.28	MUS MUSCULUS	<u>6679385</u>	65-kDa macrophage protein

## Detailed Results

11/17 matches (64%). 70149.7 Da, pI = 5.20, Acc #29840803, MUS MUSCULUS, unnamed protein product.

m/z	MH <sup>+</sup>	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	47.0831	442	449	(R)VNKPPVPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPELLLR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QEVATDVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NVMNSLCVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPTIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YYALPEDLVEVNP(K)	
1689.9700	1689.8560	67.4478	473	488	(K)ESLVGIACODINEGNR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GPRGIPAVVIDMSCLR(E)	

unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

the matched peptides cover 19% (120/627 AA's) of the protein.

## FIG. 14B

Coverage Map for This Hit (MS-Digest index #): 372720

2. 11/17 matches (64%). 70163.8 Da, pI = 5.24; Acc. # 26326929, MUS MUSCULUS, unnamed protein product.

m/z submitted	MH <sup>+</sup> matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)YVKFPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELLLR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFYTATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YYALPEDLVEVNPK(M)	
1689.9700	1689.8560	67.4478	473	488	(K)ESLVGIACODLNENR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSGLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest index #): 1174311

3. 10/17 matches (58%). 70201.8 Da, pI = 5.28; Acc. # 6679385, MUS MUSCULUS, 65-kDa macrophage protein.

m/z submitted	MH <sup>+</sup> matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(T)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)YVKFPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPEELLLR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPVDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFYTATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDER(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YYALPEDLVEVNPK(M)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVIDMSGLR(E)	

7 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900 1689.9700

The matched peptides cover 16% (104/627 AA's) of the protein.  
Coverage Map for This Hit (MS-Digest index #): 748520

## FIG. 14C

## MS-Tag Search Results

Sample ID (comment): Aps A-1 1040-AKPYLHDLR  
 Database searched: NCBI nr.51403  
 Molecular weight search (1000 - 200000 Da) selects 1421445 entries.  
 Full pI range: 1432416 entries.  
 Species search (HUMAN/RODENT) selects 224837 entries.  
 Combined molecular weight, pI and species searches select 122537 entries.  
 Number of sequences passing through parent mass filter: 1727  
 MS-Tag search selects 6 entries.  
 Parent mass: 1287.7700 (± 0.2000 Da)  
 Fragment ions used in search: 175.00, 155.28, 172.30, 301.48, 369.37, 432.69, 542.65, 633.34, 655.97, 742.67, 840.69 (± 0.70 Da)  
 Ion Types Considered: a b y n h

Search Method: Unmatched Ions: 2  
 Peptide Masses: monoisotopic  
 Digest: Trypsin  
 Max. # Missed Cleavages: 1  
 Cysteine Modified by: acrylamide  
 Peptide N-Terminus: Hydrogen (H)  
 Peptide C-Terminus: Free Acid (O H)

## Result Summary

Rank	# Unmatched Ions	Sequence	MT <sup>+</sup> Calculated (Da)	MT <sup>+</sup> Error (Da)	Protein MW (Da) <sub>pI</sub>	Species	NCBI nr.51403 Accession #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8117500	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4504965	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	63-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	31331.4 / 8.60	MUS MUSCULUS	12841863	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	16316929	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	19840803	unnamed protein product

## Detailed Results

Rank	# Unmatched Ions	Sequence	MT <sup>+</sup> Calculated (Da)	MT <sup>+</sup> Error (Da)	Protein MW (Da) <sub>pI</sub>	Species	NCBI nr.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.29	HOMO SAPIENS	8117500	696263	bA139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.20	HOMO SAPIENS	4504965	725492	lymphocyte cytosolic protein 1 (L-plastin)
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	746510	63-kDa macrophage protein
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	31331.4 / 8.60	MUS MUSCULUS	12841863	1146922	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70163.8 / 5.24	MUS MUSCULUS	16316929	1174311	unnamed protein product
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	19840803	171710	unnamed protein product

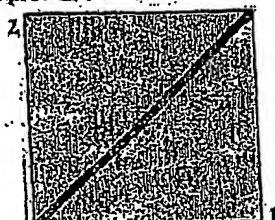
Fragment-Ion (m/z)	175.00	155.28	172.30	301.48	369.37	432.69	542.65	633.34	655.97	742.67	840.69
Ion-type	y <sub>1</sub>	y <sub>2</sub> -NH <sub>2</sub>	y <sub>2</sub>	b <sub>2</sub>	y <sub>3</sub> -NH <sub>2</sub>	b <sub>3</sub>	y <sub>4</sub>	b <sub>4</sub>	y <sub>5</sub>	y <sub>6</sub>	
Delta Da	0.12	0.13	0.13	0.33	0.18	0.52	0.34	0.09	0.58	0.21	

FIG. 15A

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 50 expect: 10.00 wordsize: 3 Filter F

Sequence 1 gi 17865718 Heat shock protein HSP 90-beta (HSP 84) (HSP 90) Length 724 (1..724)  
 Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1..724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1178 bits (3047), Expect = 0.0  
 Identities = 616/724 (85%), Positives = 616/724 (85%)

```

Query: 1  MPXXXXXXXXXXKTFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT 60
           MP          TFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT
Sbjct: 1  MPEEVHNGREEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLT 60

Query: 61  DPSKLDGKELKIDITPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG 120
           DPSKLDGKELKIDITPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG
Sbjct: 61  DPSKLDGKELKIDITPNPQERTLTLDVTGIGMTKADLINNLGTIAKSGTKAFMEALQAG 120

Query: 121 ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPICRGTK 180
           ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPICRGTK
Sbjct: 121 ADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPICRGTK 180

Query: 181 VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKXXXXXXXXXXXXXXXXXXXX 240
           VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEK
Sbjct: 181 VILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKFKREKESIDDEAEKEKERE 240

Query: 241 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDQEELNKTKEIWRNPDDITQEE 300
           IDQEELNKTKEIWRNPDDITQEE
Sbjct: 241 DKEDDEKPKIEDVGSDEEDDSGDKKKKTKKKIKKXIDQEELNKTKEIWRNPDDITQEE 300

Query: 301 YGEFYKSLTNDWSDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV 360
           YGEFYKSLTNDWSDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV
Sbjct: 301 YGEFYKSLTNDWSDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKQNNIKLYVRRV 360

Query: 361 FIMDSCELIPEYLNFIIRGVVDSDELNINISREMLQOSKILKVIKKNIVKCLELFSELA 420

```

## FIG. 15B

```

      FINDSCDELIPEYLNFIKRG SEDLPINISREMLQQSKILKVIKKNIVKKCI SELA
Sbjct: 361 FIMDSCELIPEYLNFIKRGVDSEDLPINISREMLQQSKILKVIKKNIVKKCLLDFSELA 470

Query: 421 EDKENYKKFYEAAPSNNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ 480
      EDKENYKKFYEAAPSNNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ
Sbjct: 421 EDKENYKKFYEAAPSNNLKLGIHEDSTNRRRLSELLRYHTSQSGDEMTSLSEYVSRMKETQ 480

Query: 481 KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVTXX 540
      KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVT
Sbjct: 481 KSIYYITGESKEQVANSAPVERVRKRGFEVVMTEPIDEYCVQQLKEFDGKSLSVTKEG 540

Query: 541 XXXXXXXXXXXXXXXXXXXXNLCMLKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA 600
      ; NLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA
Sbjct: 541 LRLPEDEEEKKIMRESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWA 600

Query: 601 NNERIMKAQALRDNSTMGYNMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE 660
      NNERIMKAQALRDNSTMGYNMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE
Sbjct: 601 NNERIMKAQALRDNSTMGYNMAKKHLEINPDHFIVETLRQKAEADKNDKAVKDLVLLFE 660

Query: 661 TALLSSQFSLEDPQTHSNRIYRMKLGGLIXXXXXXXXXXXXXXXXXXIPPLEGDEDASRM 720
      TALLSSQFSLEDPQTHSNRIYRMKLGGLI IPPLEGDEDASRM
Sbjct: 661 TALLSSQFSLEDPQTHSNRIYRMKLGGLIDEVTAEEPSAAVDEIPPLEGDEDASRM 720

Query: 721 EEVD 724
      EEVD
Sbjct: 721 EEVD 724

CPU time: 0.15 user secs. 0.06 sys. secs 0.21 total secs.

Lambda K H
0.317 0.115 0.375

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 4890
Number of Sequences: 0
Number of extensions: 325
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 724
length of database: 405,742,523
effective HSP length: 134
effective length of query: 590
effective length of database: 405,742,389
effective search space: 239388009510
effective search space used: 239388009510
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)

S1: 41 (21.6 bits)
S2: 78 (34.7 bits)

```

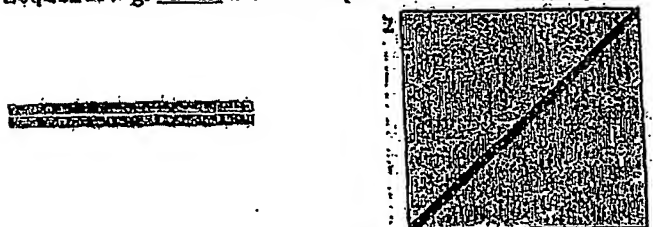
FIG. 16A

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 50 expect: 10.00 wordsize: 3 Filter: T

Sequence 1 gi 72220 heat shock protein 86 - mouse Length 733 (1..733)

Sequence 2 gi 72223 heat shock protein 84 - mouse Length 724 (1..724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0  
 Identities = 564/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

```

Query: 1  MPDETQTQDQPMEESEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIR 60
          MPDE                      BEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISN+SDALDKIR
Sbjct: 1  MPDEVRHG-----BEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIR 55

Query: 61  YESLTDPSKLDGSGKELHINLIPSKODRTLTIIVDTGIGMTKADLINNLGTIAKSGTKAFME 120
          YESLTDPSKLDGSGKEL I++IP+ Q+RTLT+VDTGIGMTKADLINNLGTIAKSGTKAFME
Sbjct: 56  YESLTDPSKLDGSGKELKIDYIPNPQERTLTIVDTGIGMTKADLINNLGTIAKSGTKAFME 115

Query: 121  ALQAGADISMIGQFGVGFSAYLVAEKVTVITKHNDEQYAWESSAGGSFTVRIDGEPM 180
          ALQAGADISMIGQFGVGFSAYLVAEKV VITKHNDEQYAWESSAGGSFTVR D GEP+
Sbjct: 116  ALQAGADISMIGQFGVGFSAYLVAEKVVVITKHNDEQYAWESSAGGSFTVRADHGEP 175

Query: 161  GRGTKVILHLKEDQTEYLEERRIKETVKKHSQFIGYPITLFVEKERXXXXXXXXXXXXX 240
          GRGTKVILHLKEDQTEYLEERR+KE+VKKHSQFIGYPITL++EKER
Sbjct: 176  GRGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREREKESDOBAEBEKG 235

Query: 241  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 300
          LNKTKPIINTR
Sbjct: 236  EKEEEDKEDEEKPKIEDVGSDEEDDSGKDKKKKTKKIKIKYIDQE-----LNKTKPIINTR 291

Query: 301  NPDDITNEEYGEFYKSLTNDNEHLAVKHFSVEGQLEFRALLFVPRRAPFDLFENKKKN 360
          NPDDIT EEEYGEFYKSLTNDWE+HLAVKHFSVEGQLEFRALLF+PRRAPFDLPEN+KKKN
Sbjct: 292  NPDDITQEEYGEFYKSLTNDWEHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKN 351

Query: 361  NIKLYVRRVFIMDNCEBLIPEYLNEIRGVVDSEDLPNISREMLQQSKILKIVIRKNLVKK 420
  
```

## FIG. 16B

```

      NIKLYVRRVFMDC+CL. :LNFIRGVVDSDDLPLNISREMLQQSKILKVI .VKK
Sbjct: 352 NIKLYVRRVFMDCDELIRSYLNFIRGVVDSDDLPLNISREMLQQSKILKVI.RNIVKK 411

Query: 421 CLELFTELAEDKENYKKPYEQPSKNIKLGIBEDSQNRKQLSELLRYTTSASGDEMVS LKD 480
      CLELF+ELAEDKENYKKPYE PSKN+KLGIBEDS NR++LSELLRY+TS SGOEM SL +
Sbjct: 412 CLELPSELAEDKENYKKPYEAFSKNLKLGIBEDSTNRRRLSELLRYHTSQSODENTSLSE 471

Query: 481 YCTRMKENQKHIFITGETKQVANSAPVERLRKHCLVYIMIEPIDEYCVQQLKEFEKG 540
      Y +RMKE QK IY+ITGS+K+QVANSAPVER+RK G EV+YM EPIDEYCVQQLKEP+CK
Sbjct: 472 YVSRMKRTQKSIYYITGESKEQVANSAPVERVRKRGFEVVYMTFTIDEYCVQQLKEFGK 531

Query: 541 TLVSVTXXXXXXXXXXXXXXXXXXXXXXXXXNLCIMKDILEKKVEKVVVSNRLVTSPPCCI 600
      +LVSVT NLCK+MK+IL+KKVEKV +SNRLV+SPCCI
Sbjct: 532 SLVSVTKEGLELPEDEEEKKKMEESKAKFENLCKLMKEI LDKKVEKVTISNRLVSSPCCI 591

Query: 601 VTSTYGTANMERIMKAQALRDNSTMGYMAAKKGLLEINPDHSIIETLRQAEADKNDKSV 660
      VTSTYGTANMERIMKAQALRDNSTMGYM AKKGLLEINPDH I+ETLRQAEADKNDK+V
Sbjct: 592 VTSTYGTANMERIMKAQALRDNSTMGYMAKIGLEINPDHPIVETLRQAEADKNDKAV 651

Query: 661 KDLVILLYETALLSSGFSLEDPQTHANRIYRMIKLGLGIDEDDPTVDDTSAAVTEEMPPL 720
      KDLV+LL+ETALLSSGFSLEDPQTH+NRIYRMIKLGLGIDED+ T ++ SAAV +E+PEL
Sbjct: 652 KDLVLLFETALLSSGFSLEDPQTHSNRIYRMIKLGLGIOEDVTAREPSAAVPDEIFPL 711

Query: 721 EGDDDTSRMEEVD 733
      EGD+O SRMEEVD
Sbjct: 712 EGDDEASRMEEVD 724

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda K H
0.316 0.134 0.372

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 5349
Number of Sequences: 0
Number of extensions: 384
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 733
length of database: 405,742,523
effective HSP length: 134
effective length of query: 599
effective length of database: 405,742,389
effective search space: 243039691011
effective search space used: 243039691011
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)

S1: 41 (21.6 bits)
S2: 78 (34.7 bits)

```